



IFW16

RAW SEQUENCE LISTING

DATE: 09/13/2004

PATENT APPLICATION: US/10/013,036A

TIME: 09:44:53

Input Set : A:\Corrected Seq. Listing.2004.08.31.txt

Output Set: N:\CRF4\09132004\J013036A.raw

5 <110> APPLICANT: Hillman, Jeffrey
 9 <120> TITLE OF INVENTION: Antimicrobial Polypeptide, Nucleic Acid, and Methods of Use
 13 <130> FILE REFERENCE: 00-1323H
 15 <140> CURRENT APPLICATION NUMBER: US 10/013,036A
 16 <141> CURRENT FILING DATE: 2001-10-30
 19 <150> PRIOR APPLICATION NUMBER: 09/361,900
 21 <151> PRIOR FILING DATE: 1999-07-27
 25 <150> PRIOR APPLICATION NUMBER: 08/871,924
 27 <151> PRIOR FILING DATE: 1997-06-10
 31 <160> NUMBER OF SEQ ID NOS: 12
 35 <170> SOFTWARE: PatentIn version 3.1
 39 <210> SEQ ID NO: 1
 41 <211> LENGTH: 1316
 43 <212> TYPE: DNA
 45 <213> ORGANISM: Streptococcus mutans
 49 <220> FEATURE:
 51 <221> NAME/KEY: CDS
 53 <222> LOCATION: (796)..(987)
 55 <223> OTHER INFORMATION:
 59 <220> FEATURE:
 61 <221> NAME/KEY: -35_signal
 63 <222> LOCATION: (738)..(742)
 65 <223> OTHER INFORMATION:



f.b

W--> 69 <220>

71 <221> NAME/KEY: -10_signal
 73 <222> LOCATION: (757)..(763)
 75 <223> OTHER INFORMATION:

W--> 79 <220>

81 <221> NAME/KEY: RBS
 83 <222> LOCATION: (784)..(791)
 85 <223> OTHER INFORMATION:

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92 attttttaaaa tttttaaaaa aaattattac ttactttcat gataagtcag tagatatgtc	120
94 tgaattagaa cattatatta atatagttga agaaataaat cctacgattg cttcaattct	180
96 taaatctaatt ttgaatcagc ttttataaag ttttagccat taaagccatc ttgataaatt	240
98 ttatatcttt catattcatt aaatgtggag ataatgaaaa agcaacggtt atgctatcgc	300
100 tgcttttttt gtgattagaa gctatgttat catggagtta tagtaatgaa acatagtgac	360
102 agttcatcct ttcttattat aaaagtggta ataagagaag tggtaaacia agagttagta	420
104 aaataatacg ttttaaccata atatttcctc ctttaattta ttataagatt caaaaaggta	480
106 atattcctat atttgcaaat atgggataaa ataattttta aaaagcagat ttgcaatttt	540
108 aaaaaaatag aggctaattg tgggtattata ttattgtaaa tatatgttta ctcagtaata	600
110 gtgatttact attacaacag attttgttgt tatcttagat atttctgcta gcattagtta	660

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112 tctgtagatg tactacttaa taagtatata attataatta tataataact attatcagat 720
114 taccgttaaa agttttctga tatgcttcta ctgaacaatt tatgttcagt tacacacatg 780
116 aaaaaggagg atatt atg tca aac aca caa tta tta gaa gtc ctt ggt act 831
117 Met Ser Asn Thr Gln Leu Leu Glu Val Leu Gly Thr
118 1 5 10
120 gaa act ttt gat gtt caa gaa gat ctc ttt gct ttt gat aca aca gat 879
121 Glu Thr Phe Asp Val Gln Glu Asp Leu Phe Ala Phe Asp Thr Thr Asp
122 15 20 25
124 act act att gtg gca agc aac gac gat cca gat act cgt ttc aaa agt 927
125 Thr Thr Ile Val Ala Ser Asn Asp Asp Pro Asp Thr Arg Phe Lys Ser
126 30 35 40
128 tgg agc ctt tgt acg cct ggt tgt gca agg aca ggt agt ttc aat agt 975
129 Trp Ser Leu Cys Thr Pro Gly Cys Ala Arg Thr Gly Ser Phe Asn Ser
130 45 50 55 60
132 tac tgt tgc tga ttgtataaaa gatttagatt gtgccgcatg ttagcggcac 1027
133 Tyr Cys Cys
136 aatcttttga tatttagaggt attaatatgt taaatacaca attattagaa gtccttggt 1087
138 ctaaaacttt tgatgttcaa gaagatttat ttgagtttaa tataacagat actattgtac 1147
140 tgcaggctag tgatagtcca gatactcata gtaggggtcc cgagcgctta gtgggaattt 1207
142 gtatcgataa ggggtacaaa ttcccactaa accaatgttt caaggcctat ttatttttta 1267
144 tattcaattc tcttaagtgt ttaggaatag ataacaagtc aaattttata 1316
147 <210> SEQ ID NO: 2
149 <211> LENGTH: 63
151 <212> TYPE: PRT
153 <213> ORGANISM: Streptococcus mutans
157 <400> SEQUENCE: 2
159 Met Ser Asn Thr Gln Leu Leu Glu Val Leu Gly Thr Glu Thr Phe Asp
160 1 5 10 15
163 Val Gln Glu Asp Leu Phe Ala Phe Asp Thr Thr Asp Thr Thr Ile Val
164 20 25 30
167 Ala Ser Asn Asp Asp Pro Asp Thr Arg Phe Lys Ser Trp Ser Leu Cys
168 35 40 45
171 Thr Pro Gly Cys Ala Arg Thr Gly Ser Phe Asn Ser Tyr Cys Cys
172 50 55 60
175 <210> SEQ ID NO: 3
177 <211> LENGTH: 1323
179 <212> TYPE: DNA
181 <213> ORGANISM: Streptococcus mutans
185 <220> FEATURE:
187 <221> NAME/KEY: CDS
189 <222> LOCATION: (228)..(782)
191 <223> OTHER INFORMATION:
195 <220> FEATURE:
197 <221> NAME/KEY: -35_signal
199 <222> LOCATION: (177)..(182)
201 <223> OTHER INFORMATION:
W--> 205 <220>
207 <221> NAME/KEY: -10_signal
209 <222> LOCATION: (191)..(196)

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211 <223> OTHER INFORMATION:

W--> 215 <220>

217 <221> NAME/KEY: RBS

219 <222> LOCATION: (218)..(224)

221 <223> OTHER INFORMATION:

W--> 225 <400> 3

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228 ttactgttgt taactataaa ttatacttaa attgatagga aacttggtcg tgacattatc      120
230 atatgttgat attggaagag aatcaaattt ataaagacaa ttaaattctaa atttgatgaa      180
232 tatttagatg aattattact aggttgacag tcatgttagg agaagag atg aac gat      236
233                                     Met Asn Asp
234                                     1
236 ttt caa ttt caa gat tat ttt atg tac aga aaa cca tta ggc aac ttt      284
237 Phe Gln Phe Gln Asp Tyr Phe Met Tyr Arg Lys Pro Leu Gly Asn Phe
238      5              10              15
240 tct aat ttt ttt agt ata act gat acg atg gat ccc att gag tta cta      332
241 Ser Asn Phe Phe Ser Ile Thr Asp Thr Met Asp Pro Ile Glu Leu Leu
242 20              25              30              35
244 cat agt gat ccg ata ttt gct gaa gga gta tat ttg gcc tct tca tct      380
245 His Ser Asp Pro Ile Phe Ala Glu Gly Val Tyr Leu Ala Ser Ser Ser
246              40              45              50
248 ctt aga gca gcc ata aat aaa ctt aag aat cat act gcg agt act aag      428
249 Leu Arg Ala Ala Ile Asn Lys Leu Lys Asn His Thr Ala Ser Thr Lys
250              55              60              65
252 gat aaa aag aat gca aga gag act att ttt caa tac tat gcc cgt tat      476
253 Asp Lys Lys Asn Ala Arg Glu Thr Ile Phe Gln Tyr Tyr Ala Arg Tyr
254              70              75              80
256 aac acg aga tca act ccg ttt ggc ttg ttt tcg tcc atc gga gta ggt      524
257 Asn Thr Arg Ser Thr Pro Phe Gly Leu Phe Ser Ser Ile Gly Val Gly
258      85              90              95
260 gct ttt tcg gct tac ctt aaa aaa gaa aag tct cgt tat gaa aaa tct      572
261 Ala Phe Ser Ala Tyr Leu Lys Lys Glu Lys Ser Arg Tyr Glu Lys Ser
262 100              105              110              115
264 att aat att gat ctt ttt tgg gct tat aaa gta gca gat aaa cta gaa      620
265 Ile Asn Ile Asp Leu Phe Trp Ala Tyr Lys Val Ala Asp Lys Leu Glu
266              120              125              130
268 agt atg cct gaa att tta aat act tta aaa gta gtt gct aat aat gct      668
269 Ser Met Pro Glu Ile Leu Asn Thr Leu Lys Val Val Ala Asn Asn Ala
270              135              140              145
272 ttg caa aag tca gat aat ttt tgg ctt ttg gat acg cga agt cat ttt      716
273 Leu Gln Lys Ser Asp Asn Phe Trp Leu Leu Asp Thr Arg Ser His Phe
274              150              155              160
276 ggt ctt atg aat tct ttt cat ttt atc ttg tac gac ttc tat tct ttc      764
277 Gly Leu Met Asn Ser Phe His Phe Ile Leu Tyr Asp Phe Tyr Ser Phe
278      165              170              175
280 ctt caa gat aga cca taa gaattgatat atcagctgga ttcacaccag      812
281 Leu Gln Asp Arg Pro
282 180
284 aaatacggct agcttgacca atagtttctg gggttaatttt cttaaatttc tgacgtgctt      872

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286 cggtcgcaat agaatcaatg gcatcccaat cgatattctt aggaattcga gctcgggtacc 932
288 cggggatcct ctagagtcga cctgcaggca tgcaagcttg gcactggccg tcgtttttaca 992
290 acgtcgtgac tgggaaaacc ctggcggttac ccaacttaat cgccttgacg cacatccccc 1052
292 ttctgccagc tggcgtaata gcgaagaggc ccgcaccgat cgccttccc aacagttgcg 1112
294 cagcctgaat ggcgaatggc gcctgatgcg gtattttctc cttacgcac tgtgcggtat 1172
296 ttcacaccgc atatggtgca ctctcagtac aatctgctct gatgccgat agttaagcca 1232
298 gccccgacac ccgccaacac ccgctgacgc gccctgacgg gcttgtctgc tcccggcatc 1292
300 cgcttacaga caagctgtga ccgtctccgg g 1323

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303 <210> SEQ ID NO: 4

305 <211> LENGTH: 184

307 <212> TYPE: PRT

309 <213> ORGANISM: Streptococcus mutans

313 <400> SEQUENCE: 4

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315 Met Asn Asp Phe Gln Phe Gln Asp Tyr Phe Met Tyr Arg Lys Pro Leu
316 1 5 10 15
319 Gly Asn Phe Ser Asn Phe Phe Ser Ile Thr Asp Thr Met Asp Pro Ile
320 20 25 30
323 Glu Leu Leu His Ser Asp Pro Ile Phe Ala Glu Gly Val Tyr Leu Ala
324 35 40 45
327 Ser Ser Ser Leu Arg Ala Ala Ile Asn Lys Leu Lys Asn His Thr Ala
328 50 55 60
331 Ser Thr Lys Asp Lys Lys Asn Ala Arg Glu Thr Ile Phe Gln Tyr Tyr
332 65 70 75 80
335 Ala Arg Tyr Asn Thr Arg Ser Thr Pro Phe Gly Leu Phe Ser Ser Ile
336 85 90 95
339 Gly Val Gly Ala Phe Ser Ala Tyr Leu Lys Lys Glu Lys Ser Arg Tyr
340 100 105 110
343 Glu Lys Ser Ile Asn Ile Asp Leu Phe Trp Ala Tyr Lys Val Ala Asp
344 115 120 125
347 Lys Leu Glu Ser Met Pro Glu Ile Leu Asn Thr Leu Lys Val Val Ala
348 130 135 140
351 Asn Asn Ala Leu Gln Lys Ser Asp Asn Phe Trp Leu Leu Asp Thr Arg
352 145 150 155 160
355 Ser His Phe Gly Leu Met Asn Ser Phe His Phe Ile Leu Tyr Asp Phe
356 165 170 175

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359 Tyr Ser Phe Leu Gln Asp Arg Pro

360 180

363 <210> SEQ ID NO: 5

365 <211> LENGTH: 22

367 <212> TYPE: PRT

369 <213> ORGANISM: Streptococcus mutans

373 <220> FEATURE:

375 <221> NAME/KEY: MISC_FEATURE

377 <222> LOCATION: (3)..(3)

379 <223> OTHER INFORMATION: 2,3-didehydroalanine

383 <220> FEATURE:

385 <221> NAME/KEY: MISC_FEATURE

387 <222> LOCATION: (5)..(5)

389 <223> OTHER INFORMATION: alanyl moiety of lanthionine

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393 <220> FEATURE:
395 <221> NAME/KEY: MISC_FEATURE
397 <222> LOCATION: (7)..(7)
399 <223> OTHER INFORMATION: alanyl moiety of lanthionine
403 <220> FEATURE:
405 <221> NAME/KEY: MISC_FEATURE
407 <222> LOCATION: (11)..(11)
409 <223> OTHER INFORMATION: alanyl moiety of lanthionine
413 <220> FEATURE:
415 <221> NAME/KEY: MISC_FEATURE
417 <222> LOCATION: (16)..(16)
419 <223> OTHER INFORMATION: alanyl moiety of lanthionine
423 <220> FEATURE:
425 <221> NAME/KEY: MISC_FEATURE
427 <222> LOCATION: (19)..(19)
429 <223> OTHER INFORMATION: alanyl moiety of lanthionine
433 <220> FEATURE:
435 <221> NAME/KEY: MISC_FEATURE
437 <222> LOCATION: (21)..(21)
439 <223> OTHER INFORMATION: alanyl moiety of lanthionine
443 <220> FEATURE:
445 <221> NAME/KEY: MISC_FEATURE
447 <222> LOCATION: (8)..(8)
449 <223> OTHER INFORMATION: 2,3-didehydrobutyrine
453 <220> FEATURE:
455 <221> NAME/KEY: MISC_FEATURE
457 <222> LOCATION: (14)..(14)
459 <223> OTHER INFORMATION: S-2-aminobutyric acid
463 <220> FEATURE:
465 <221> NAME/KEY: MISC_FEATURE
467 <222> LOCATION: (22)..(22)
469 <223> OTHER INFORMATION: S-[aminovinyl]-cysteine
473 <220> FEATURE:
475 <221> NAME/KEY: THIOETH
477 <222> LOCATION: (5)..(7)
479 <223> OTHER INFORMATION:
483 <220> FEATURE:
485 <221> NAME/KEY: THIOETH
487 <222> LOCATION: (11)..(14)
489 <223> OTHER INFORMATION:
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495 <221> NAME/KEY: THIOETH
497 <222> LOCATION: (16)..(21)
499 <223> OTHER INFORMATION:
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505 <221> NAME/KEY: THIOETH
507 <222> LOCATION: (19)..(22)
509 <223> OTHER INFORMATION:
W--> 513 <400> 5

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/13/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:6; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:7; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:8; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:9; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:10; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:11; Xaa Pos. 3,5,7,8,11,14,16,19,21,22

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Input Set : A:\Corrected Seq. Listing.2004.08.31.txt

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L:69 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:55
L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:65
L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:75
L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:85
L:205 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:191
L:215 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:201
L:225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:211
L:225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:221
L:493 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:479
L:503 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:489
L:513 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:499
L:513 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:509
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
L:653 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:639
L:663 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:649
L:673 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:659
L:673 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:669
L:675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16
L:813 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:799
L:823 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:809
L:833 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:819
L:833 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:829
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:16
L:973 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:959
L:983 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:969
L:993 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:979
L:993 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:989
L:995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
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L:1133 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1119
L:1143 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1129
L:1153 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1139
L:1153 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1149
L:1155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
L:1293 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1279
L:1303 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1289
L:1313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1299
L:1313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1309
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:1319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16
L:1443 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1429
L:1453 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1439
L:1463 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1449
L:1473 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1459

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L:1475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16